

SEQUENCE LISTING

<110> Tang, Y. Tom

Zhou, Ping

Goodrich, Ryle

Liu, Chenghua

Asundi, Vinod

Ren, Feiyan

Zhao, Qing A.

Yang, Yonghong

Wehrman, Tom

Drmanac, Radoje T.

<120> Novel Nucleic Acids and
Polypeptides

<130> 787CIP2F

<140> To Be Assigned

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<150> 09/560,875

<151> 2000-04-27

<150> 09/496,914

<151> 2000-02-03

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gtaacttgcc	tcatagtcat	tttcttggaa	attcaatttc	ttctccacag	ggtctcttt	360
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gatccttgtt	tttattaccc	tatcattaat	gttttctgtt	ttcctttatc	agcgagttac	480
tgctcatttg	attcatattg	ccaaactgaa	ctctcttgc	ttcttgcaag	atgaaaggag	540
acaacc	atg aat gag cca cta gac tat tta gca aat gct tct gat ttc					588
	Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe					
1	5	10				
ccc	gat tat gca gct gct ttt gga aat tgc act gat gaa aac atc cca					636
Pro Asp Tyr Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro						
15	20	25	30			
ctc	aag atg cac tac ctc cct gtt att tat ggc att atc ttc ctc gtg					684
Leu Lys Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val						
35	40	45				
gga	ttt cca ggc aat gca gta gtg ata tcc act tac att ttc aaa atg					732
Gly Phe Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met						
50	55	60				
aga	cct tgg aag agc agc acc atc att atg ctg aac ctg gcc tgc aca					780
Arg Pro Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr						
65	70	75				
gat	ctg ctg tat ctg acc agc ctc ccc ttc ctg att cac tac tat gcc					828
Asp Leu Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala						
80	85	90				
agt	ggc gaa aac tgg atc ttt gga gat ttc atg tgt aag ttt atc cgc					876
Ser Gly Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg						
95	100	105	110			
ttc	agc ttc cat ttc aac ctg tat agc agc atc ctc ttc ctc acc tgt					924
Phe Ser Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys						
115	120	125				
ttc	agc atc ttc cgc tac tgt gtg atc att cac cca atg agc tgc ttt					972
Phe Ser Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe						
130	135	140				
tcc	att cac aaa act cga tgt gca gtt gta gcc tgt gct gtg gtg tgg					1020
Ser Ile His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp						
145	150	155				
atc	att tca ctg gta gct gtc att ccg atg acc ttc ttg atc aca tca					1068
Ile Ile Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser						
160	165	170				

acc aac agg acc aac aga tca gcc tgt ctc gac ctc acc agt tcg gat			1116
Thr Asn Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp			
175	180	185	190
gaa ctc aat act att aag tgg tac aac cta att ttg act gca act act			1164
Glu Leu Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr			
195	200	205	
ttg cct ccc ctt ggt gat agt gac act ttg cta tac cac gat tat cca			1212
Leu Pro Pro Leu Gly Asp Ser Asp Thr Leu Leu Tyr His Asp Tyr Pro			
210	215	220	
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His Ser Asp Pro Trp Thr Ala Asn *			
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Ala Ala Leu Asp Pro Ala Tyr Thr Leu Glu Phe Glu Asn Val Gln			
20	25	30	

gtg ttg acg atg ggc aat gac acg tcc cca tca gaa ggc acc aac ctc		201	
Val Leu Thr Met Gly Asn Asp Thr Ser Pro Ser Glu Gly Thr Asn Leu			
35	40	45	

aac gcg ccc aac agc ctg ggt gtc agc gcc ctg tgt gcc atc tgc ggg		249	
Asn Ala Pro Asn Ser Leu Gly Val Ser Ala Leu Cys Ala Ile Cys Gly			
50	55	60	

gac cgg gcc acg ggc aaa cac tac ggt gcc tcg agc tgt gac ggc tgc		297	
Asp Arg Ala Thr Gly Lys His Tyr Gly Ala Ser Ser Cys Asp Gly Cys			
65	70	75	80

aag ggc ttc ttc cgg agg agc gtg cgg aag aac cac atg tac tcc tgc		345	
Lys Gly Phe Phe Arg Arg Ser Val Arg Lys Asn His Met Tyr Ser Cys			
85	90	95	

aga ttt agc cgg cag tgc gtg gac aaa gac aag agg aac cag tgc		393
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Arg Phe Ser Arg Gln Cys Val Val Asp Lys Asp Lys Arg Asn Gln Cys			
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cgc tac tgc agg ctc aag aaa tgc ttc cgg gct ggc atg aag aag gaa			441
Arg Tyr Cys Arg Leu Lys Lys Cys Phe Arg Ala Gly Met Lys Lys Glu			
115	120	125	
gcc gtc cag aat gag cgg gac cgg atc agc act cga agg tca agc tat			489
Ala Val Gln Asn Glu Arg Asp Arg Ile Ser Thr Arg Arg Ser Ser Tyr			
130	135	140	
gag gac agc agc ctg ccc tcc atc aat gcg ctc ctg cag gcg gag gtc			537
Glu Asp Ser Ser Leu Pro Ser Ile Asn Ala Leu Leu Gln Ala Glu Val			
145	150	155	160
ctg tcc cga cag atc acc tcc ccc gtc tcc ggg atc aac ggc gac att			585
Leu Ser Arg Gln Ile Thr Ser Pro Val Ser Gly Ile Asn Gly Asp Ile			
165	170	175	
cgg gcg aag aag att gcc agc atc gca gat gtg tgt gag tcc atg aag			633
Arg Ala Lys Lys Ile Ala Ser Ile Ala Asp Val Cys Glu Ser Met Lys			
180	185	190	
gag cag ctg ctg gtt ctc gag tgg gcc aag tac atc cca gct ttc			681
Glu Gln Leu Leu Val Leu Val Glu Trp Ala Lys Tyr Ile Pro Ala Phe			
195	200	205	
tgc gag ctc ccc ctg gac cag gtg gcc ctg ctc aga gcc cat gct			729
Cys Glu Leu Pro Leu Asp Asp Gln Val Ala Leu Leu Arg Ala His Ala			
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ggc gag cac ctg ctg ctc gga gcc acc aag aga tcc atg gtg ttc aag			777
Gly Glu His Leu Leu Leu Gly Ala Thr Lys Arg Ser Met Val Phe Lys			
225	230	235	240
gac gtg ctg ctc cta ggc aat gac tac att gtc cct cgg cac tgc ccg			825
Asp Val Leu Leu Leu Gly Asn Asp Tyr Ile Val Pro Arg His Cys Pro			
245	250	255	
gag ctg gcg gag atg agc cgg gtg tcc ata cgc atc ctt gac gag ctg			873
Glu Leu Ala Glu Met Ser Arg Val Ser Ile Arg Ile Leu Asp Glu Leu			
260	265	270	
gtg ctg ccc ttc cag gag ctg cac atc gat gac aat gag tat gcc tac			921
Val Leu Pro Phe Gln Glu Leu His Ile Asp Asp Asn Glu Tyr Ala Tyr			
275	280	285	
ctc aaa gcc atc atc ttc ttt gac cca gat gcc aag ggg ctg agc gat			969
Leu Lys Ala Ile Ile Phe Phe Asp Pro Asp Ala Lys Gly Leu Ser Asp			
290	295	300	
cca ggg aag atc aag cgg ctg cgt tcc cag gtg cag gtg agc ttg gag			1017
Pro Gly Lys Ile Lys Arg Leu Arg Ser Gln Val Gln Val Ser Leu Glu			
305	310	315	320
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Asp Tyr Ile Asn Asp Arg Gln Tyr Asp Ser Arg Gly Arg Phe Gly Glu			

325	330	335								
ctg ctg ctg ctg ccc acc ttg cag agc atc acc tgg cag atg atc Leu Leu Leu Leu Pro Thr Leu Gln Ser Ile Thr Trp Gln Met Ile 340	345	350	1113							
gag cag atc cag ttc atc aag ctc ttc ggc atg gcc aag att gac aac Glu Gln Ile Gln Phe Ile Lys Leu Phe Gly Met Ala Lys Ile Asp Asn 355	360	365	1161							
ctg ttg cag gag atg ctg ctg gga ggg tcc ccc agc gat gca ccc cat Leu Leu Gln Glu Met Leu Leu Gly Gly Ser Pro Ser Asp Ala Pro His 370	375	380	1209							
gcc cac cac ccc ctg cac cct cac ctg atg cag gaa cat atg gga acc Ala His His Pro Leu His Pro His Leu Met Gln Glu His Met Gly Thr 385	390	395	1257							
aac gtc atc gtt gcc aac aca atg ccc act cac ctc agc aac gga cag Asn Val Ile Val Ala Asn Thr Met Pro Thr His Leu Ser Asn Gly Gln 405	410	415	1305							
atg tgt gag tgg ccc cga ccc agg gga cag gca gcc acc cct gag acc Met Cys Glu Trp Pro Arg Pro Arg Gly Gln Ala Ala Thr Pro Glu Thr 420	425	430	1353							
cca cag ccc tca ccg cca ggt ggc tca ggg tct gag ccc tat aag ctc Pro Gln Pro Ser Pro Pro Gly Gly Ser Gly Ser Glu Pro Tyr Lys Leu 435	440	445	1401							
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465										
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 aggcaaggca ctgaagggtt taagtcccct ggggctggat tccgccttcc ggctttccc 180
 agacccaga gccggtccct ggaacactgc agtccctgagc tctggg atg gag ccc 235
 Met Glu Pro
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gag act gcg ctg tgg ggc ccg gat ctg cag ggt ccg gaa cag agc ccc 283
 Glu Thr Ala Leu Trp Gly Pro Asp Leu Gln Gly Pro Glu Gln Ser Pro
 5 10 15

aac gat gct cac aga ggt gcc gag agt gaa aac gaa gag gag agc cct 331
 Asn Asp Ala His Arg Gly Ala Glu Ser Glu Asn Glu Glu Glu Ser Pro
 20 25 30 35

cggtttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 379
 Arg Gln Glu Ser Ser Gly Glu Glu Ile Ile Met Gly Asp Pro Ala Gln
 40 45 50

agt cca gaa tcc aag gac tca aca gag atg tcc ctg gag aga tcc tcc		427
Ser Pro Glu Ser Lys Asp Ser Thr Glu Met Ser Leu Glu Arg Ser Ser		
55	60	65
cag gac ccc tct gtc ccc cag aac ccc cca acc cca ctg ggt cac tcc		475
Gln Asp Pro Ser Val Pro Gln Asn Pro Pro Thr Pro Leu Gly His Ser		
70	75	80
aat ccc ttg gac cac cag atc ccc ctg gac ccc cca gcc ccg gag gta		523
Asn Pro Leu Asp His Gln Ile Pro Leu Asp Pro Pro Ala Pro Glu Val		
85	90	95
gtc cct acc cca tct gac tgg acc aag gcc tgc gag gcc agc tgg cag		571
Val Pro Thr Pro Ser Asp Trp Thr Lys Ala Cys Glu Ala Ser Trp Gln		
100	105	110
115		
tgg ggc gct ctc acc aca tgg aac agc ccc cca gtc gtc ccc gcc aac		619
Trp Gly Ala Leu Thr Thr Trp Asn Ser Pro Pro Val Val Pro Ala Asn		
120	125	130
gag ccc agc ctg cgg gag ctg gtg cag ggc cgc ccg gcg ggg gcg gag		667
Glu Pro Ser Leu Arg Glu Leu Val Gln Gly Arg Pro Ala Gly Ala Glu		
135	140	145
aag ccc tac atc tgc aac gag tgc ggc aag agc ttc agc cag tgg tcc		715
Lys Pro Tyr Ile Cys Asn Glu Cys Gly Lys Ser Phe Ser Gln Trp Ser		
150	155	160
aag ctg ctg cgg cac cag cgc atc cac acg gga gag cgg ccc aac acc		763
Lys Leu Leu Arg His Gln Arg Ile His Thr Gly Glu Arg Pro Asn Thr		
165	170	175
tgc tcc gag tgc ggc aag agc ttc acg cag agc tcg cac ctg gtg cag		811
Cys Ser Glu Cys Gly Lys Ser Phe Thr Gln Ser Ser His Leu Val Gln		
180	185	190
195		
cac cag cgc acg cac acc ggc gag aag ccc tac aag tgc ccc gac tgc		859
His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Asp Cys		
200	205	210
ggc aag tgc ttc agc tgg agc tcc aac ctg gtg cag cac cag cgc acg		907
Gly Lys Cys Phe Ser Trp Ser Ser Asn Leu Val Gln His Gln Arg Thr		
215	220	225
cac acg gga gaa gag ccc tac aag tgc acg gag tgc gag ata gcc ttc		955
His Thr Gly Glu Pro Tyr Lys Cys Thr Glu Cys Glu Ile Ala Phe		
230	235	240
acc cag agc acc aac ctc atc aag cac cag cga tcc cac acc ggc gag		1003
Thr Gln Ser Thr Asn Leu Ile Lys His Gln Arg Ser His Thr Gly Glu		
245	250	255
aag ccc tac aag tgc ggc gag tgc cgc cgg gct ttc tac cgc agc tgc		1051
Lys Pro Tyr Lys Cys Gly Glu Cys Arg Arg Ala Phe Tyr Arg Ser Ser		
260	265	270
275		

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Asp Leu Ile Gln His Gln Ala Thr His Thr Gly Glu Lys Pro Tyr Lys			
280	285	290	
tgc ccc gag tgc ggg aag cgc ttc ggc cag aac cac aac ctc ctc aag			1147
Cys Pro Glu Cys Gly Lys Arg Phe Gly Gln Asn His Asn Leu Leu Lys			
295	300	305	
cac cag aag atc cac gcg ggc gag aag cca tac cgc tgc acc gag tgc			1195
His Gln Lys Ile His Ala Gly Glu Lys Pro Tyr Arg Cys Thr Glu Cys			
310	315	320	
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Gly Lys Ser Phe Ile Gln Ser Ser Glu Leu Thr Gln His Gln Arg Thr			
325	330	335	
cac aca ggc gag aag ccc tac gag tgc cta gag tgc ggc aag agc ttc			1291
His Thr Gly Glu Lys Pro Tyr Glu Cys Leu Glu Cys Gly Lys Ser Phe			
340	345	350	355
ggc cac agc tcc acc ctc atc aag cac cag cgg act cac ctg cgc gag			1339
Gly His Ser Ser Thr Leu Ile Lys His Gln Arg Thr His Leu Arg Glu			
360	365	370	
gac ccg ttc aag tgc cca gtg tgc ggc aag acc ttc acc ctg agc gcc			1387
Asp Pro Phe Lys Cys Pro Val Cys Gly Lys Thr Phe Thr Leu Ser Ala			
375	380	385	
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Thr Leu Leu Arg His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys			
390	395	400	
tgc cca gag tgc ggc aag agc ttc agc gtc agc tcc aac ctc atc aac			1483
Cys Pro Glu Cys Gly Lys Ser Phe Ser Val Ser Ser Asn Leu Ile Asn			
405	410	415	
cac cag cgc atc cac cgc ggc gag cgg ccc tac atc tgc gcc gac tgc			1531
His Gln Arg Ile His Arg Gly Glu Arg Pro Tyr Ile Cys Ala Asp Cys			
420	425	430	435
ggc aag agc ttc atc atg agc tcc acc ctt atc cgc cac cag cgc atc			1579
Gly Lys Ser Phe Ile Met Ser Ser Thr Leu Ile Arg His Gln Arg Ile			
440	445	450	
cac acc ggt gag aag ccc tac aag tgt tcc gac tgc ggc aag agc ttc			1627
His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Asp Cys Gly Lys Ser Phe			
455	460	465	
atc cgc agc tcc cac ctt atc cag cac cgc cgc acg cac acc ggc gag			1675
Ile Arg Ser Ser His Leu Ile Gln His Arg Arg Thr His Thr Gly Glu			
470	475	480	
aag ccc tac aag tgc ccc gag tgc ggc aag agc ttc agc cag agc tcc			1723
Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser			
485	490	495	
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Asn Leu Ile Thr His Val Arg Thr His Met Asp Glu Asn Leu Phe Val			
500	505	510	515
tgc tcc gac tgc ggg aag gcc ttc ctg gaa gcc cac gag ctg gag cag			1819
Cys Ser Asp Cys Gly Lys Ala Phe Leu Glu Ala His Glu Leu Glu Gln			
520	525		530
cac cgg gtg atc cat gag agg ggg aag acc cca gcg cgt agg gcc cag			1867
His Arg Val Ile His Glu Arg Gly Lys Thr Pro Ala Arg Arg Ala Gln			
535	540		545
ggc gac agc ctg ctg ggg ctc ggg gac ccc tcc ctg ctg acc ccg ccg			1915
Gly Asp Ser Leu Leu Gly Leu Gly Asp Pro Ser Leu Leu Thr Pro Pro			
550	555		560
ccg gga gcc aag ccg cac aag tgt ctc gtg tgc gga aag ggc ttc aac			1963
Pro Gly Ala Lys Pro His Lys Cys Leu Val Cys Gly Lys Gly Phe Asn			
565	570		575
gac gag ggc atc ttc atg caa cat cag agg atc cac atc gga gaa aac			2011
Asp Glu Gly Ile Phe Met Gln His Gln Arg Ile His Ile Gly Glu Asn			
580	585		595
ccc tac aaa aat gca gac ggc ctc atc gca cac gca gcc ccc aaa cct			2059
Pro Tyr Lys Asn Ala Asp Gly Leu Ile Ala His Ala Ala Pro Lys Pro			
600	605		610
cct cag tta cga tcc cca agg ctc cct ttc aga ggg aat tcc tac ccc			2107
Pro Gln Leu Arg Ser Pro Arg Leu Pro Phe Arg Gly Asn Ser Tyr Pro			
615	620		625
ggg gct gcg gag ggc aga gcg gag gcc ccc gga cag ccc ctt aag ccg			2155
Gly Ala Ala Glu Gly Arg Ala Glu Ala Pro Gly Gln Pro Leu Lys Pro			
630	635		640
ccg gag ggt cag gag ggc ttc agc cag agg cgg ggg ctg ctg tcc tcc			2203
Pro Glu Gly Gln Glu Gly Phe Ser Gln Arg Arg Gly Leu Leu Ser Ser			
645	650		655
aag acc tac atc tgc tcc cac tgc gga gag agc ttc ctg gat cgc tct			2251
Lys Thr Tyr Ile Cys Ser His Cys Gly Glu Ser Phe Leu Asp Arg Ser			
660	665		675
gtg ctc ctc cag cat cag ctc acc cac ggc aac gaa aag ccc ttt ctc			2299
Val Leu Leu Gln His Gln Leu Thr His Gly Asn Glu Lys Pro Phe Leu			
680	685		690
ttt cct gat tat aga att ggc cta ggg gaa ggc gca ggg ccc agc ccc			2347
Phe Pro Asp Tyr Arg Ile Gly Leu Gly Glu Ala Gly Pro Ser Pro			
695	700		705
ttc tta agt ggg aag ccc ttt aaa tgc cct gaa tgc aaa caa agc ttt			2395
Phe Leu Ser Gly Lys Pro Phe Lys Cys Pro Glu Cys Lys Gln Ser Phe			
710	715		720
ggc ctc agc tct gag ctg ctg cac cag aaa gtc cat gca ggc ggg			2443
Gly Leu Ser Ser Glu Leu Leu His Gln Lys Val His Ala Gly Gly			

725	730	735														
aag	agc	tcc	cag	aag	agt	cca	gag	ctg	ggg	aag	agc	tct	tcc	gtc	ctc	2491
Lys	Ser	Ser	Gln	Lys	Ser	Pro	Glu	Leu	Gly	Lys	Ser	Ser	Ser	Val	Leu	
740				745				750						755		
ctg	gag	cat	ctc	agg	agc	ccc	ctg	ggg	gcc	aga	ccc	tac	cgc	tgc	tca	2539
Leu	Glu	His	Leu	Arg	Ser	Pro	Leu	Gly	Ala	Arg	Pro	Tyr	Arg	Cys	Ser	
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gat	tgc	agg	gcc	tcc	ttc	ctc	gac	cgc	gtg	gcc	ctc	acc	cgg	cac	caa	2587
Asp	Cys	Arg	Ala	Ser	Phe	Leu	Asp	Arg	Val	Ala	Leu	Thr	Arg	His	Gln	
				775				780						785		
gaa	acc	cac	acc	cag	gaa	aaa	ccc	ccc	aat	ccc	gag	gac	ccc	cct	cca	2635
Glu	Thr	His	Thr	Gln	Glu	Lys	Pro	Pro	Asn	Pro	Glu	Asp	Pro	Pro	Pro	
				790				795						800		
gag	gca	gtc	acc	ctg	tcc	aca	gat	cag	gaa	ggt	gag	ggc	gag	acc	cct	2683
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Ile Asn Glu Asp Thr Arg Val His Gly Leu Ala Leu Gln Ile Ser Glu	
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Arg Ala Ser Ser Pro Leu Ser Asn Asn His Pro Pro Thr Pro Lys Arg	
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Arg Gly Ser Gly Arg Phe Pro Arg Gln Pro Gly Arg Glu Lys Gly Pro	
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Ile Lys Glu Val Pro Gly Thr Lys Gly Ser Pro *	
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Tyr Arg Arg Ile Gly Asn Val Gly Ile Val Met Ser Leu Glu Gln Ile	
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Lys Gly Ile Glu Asp Tyr Asn Leu Leu Ala Gly His Leu Ala Met Phe	
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Pro Ile Ala Ala Leu Glu Met Arg Arg Asp Leu Gln His Trp Asp Ser	
80 85 90	

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Ala Leu Gln Leu Ala Lys His Leu Ala Pro Asp Gln Ile Pro Phe Ile	
95 100 105 110	

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Ser Lys Glu Tyr Ala Ile Gln Leu Glu Phe Ala Gly Asp Tyr Val Asn	
115 120 125	

gct ttg gct cat tat gag aaa gga ata aca ggt gat aat aag gaa cat	434
Ala Leu Ala His Tyr Glu Lys Gly Ile Thr Gly Asp Asn Lys Glu His	
130 135 140	

gat gaa gct tgt ctg gct gga gtg gcc cag atg tcc ata aga atg gga	482
Asp Glu Ala Cys Leu Ala Gly Val Ala Gln Met Ser Ile Arg Met Gly	

145	150	155	
gac ata cgt cga ggg gtt aac caa gcc ctc aag cat ccc agc agg gtc Asp Ile Arg Arg Gly Val Asn Gln Ala Leu Lys His Pro Ser Arg Val			530
160	165	170	
ctt aaa aga gac tgt gga gcc ata ttg gag aat atg aag caa ttt tca Leu Lys Arg Asp Cys Gly Ala Ile Leu Glu Asn Met Lys Gln Phe Ser			578
175	180	185	190
gaa gcg gcc caa ctg tat gaa aaa ggt ctc tac tac gat aaa gca gca Glu Ala Ala Gln Leu Tyr Glu Lys Gly Leu Tyr Tyr Asp Lys Ala Ala			626
195	200	205	
tct gtt tac atc cgc tct aag aat tgg gca aaa gtt ggt gat ctt ctg Ser Val Tyr Ile Arg Ser Lys Asn Trp Ala Lys Val Gly Asp Leu Leu			674
210	215	220	
ccc cac gtt tct cct aag atc cat ttg cag tat gcc aaa gcc aag Pro His Val Ser Ser Pro Lys Ile His Leu Gln Tyr Ala Lys Ala Lys			722
225	230	235	
gaa gca gat gga aga tac aaa gaa gct gtt gta gct tat gaa aat gca Glu Ala Asp Gly Arg Tyr Lys Glu Ala Val Val Ala Tyr Glu Asn Ala			770
240	245	250	
aaa cag tgg caa agt gta atc cgc atc tat ctg gat cac ctc aat aat Lys Gln Trp Gln Ser Val Ile Arg Ile Tyr Leu Asp His Leu Asn Asn			818
255	260	265	270
cct gaa aaa gct gtc aat att gtt aga gag acc cag tct ctg gat gga Pro Glu Lys Ala Val Asn Ile Val Arg Glu Thr Gln Ser Leu Asp Gly			866
275	280	285	
gcc aaa atg gta gcc agg ttt ttt cta cag ctt ggt gac tat ggg tct Ala Lys Met Val Ala Arg Phe Phe Leu Gln Leu Gly Asp Tyr Gly Ser			914
290	295	300	
gcc atc cag ttt ctt gtc atg tcc aaa tgc aac aat gaa gct ttc aca Ala Ile Gln Phe Leu Val Met Ser Lys Cys Asn Asn Glu Ala Phe Thr			962
305	310	315	
ctg gct cag caa cac aac aaa atg gaa atc tat gca gat att att ggt Leu Ala Gln Gln His Asn Lys Met Glu Ile Tyr Ala Asp Ile Ile Gly			1010
320	325	330	
tct gaa gac act act aat gaa gac tat caa agc att gcc tta tac ttt Ser Glu Asp Thr Thr Asn Glu Asp Tyr Gln Ser Ile Ala Leu Tyr Phe			1058
335	340	345	350
gaa gga gaa aag aga tat ctt cag gct gga aaa ttc ttc ttg ctg tgt Glu Gly Glu Lys Arg Tyr Leu Gln Ala Gly Lys Phe Phe Leu Leu Cys			1106
355	360	365	
ggc caa tat tca cga gca ctt aaa cac ttc ctg aaa tgc cca agc tcg Gly Gln Tyr Ser Arg Ala Leu Lys His Phe Leu Lys Cys Pro Ser Ser			1154
370	375	380	

gaa gat aat gtg gca ata gaa atg gca att gaa act gtt ggt cag gcc Glu Asp Asn Val Ala Ile Glu Met Ala Ile Glu Thr Val Gly Gln Ala 385 390 395	1202
aaa gat gaa ctg ctg acc aat cag ctg ata gac cat ctc ctg ggg gag Lys Asp Glu Leu Leu Thr Asn Gln Leu Ile Asp His Leu Leu Gly Glu 400 405 410	1250
aac gat agc atg cct aag gat gcc aag tac ctg ttc cgc ttg tac atg Asn Asp Ser Met Pro Lys Asp Ala Lys Tyr Leu Phe Arg Leu Tyr Met 415 420 425 430	1298
gct ctg aag caa tac cga gaa gct gcc cag act gcc atc atc att gcc Ala Leu Lys Gln Tyr Arg Glu Ala Ala Gln Thr Ala Ile Ile Ala 435 440 445	1346
aga gaa gag cag tct gca ggc aac tac cgg aat gca cac gat gtt ctc Arg Glu Glu Gln Ser Ala Gly Asn Tyr Arg Asn Ala His Asp Val Leu 450 455 460	1394
ttc agt atg tat gca gaa ctg aaa tcc cag aag atc aaa att ccc tcc Phe Ser Met Tyr Ala Glu Leu Lys Ser Gln Lys Ile Lys Ile Pro Ser 465 470 475	1442
gag atg gcc acc aac ctc atg att ctg cac agc tat ata cta gta aga Glu Met Ala Thr Asn Leu Met Ile Leu His Ser Tyr Ile Leu Val Arg 480 485 490	1490
ttc atg tta aaa atg gag atc aca tga aaggg gctcgcatgc tcattcgggt Phe Met Leu Lys Met Glu Ile Thr *	1542
495 500	
ggccaacaac atcagcaaat ttccatcaca cattgtaccc atcctgacgt caactgtgat	1602
tgagtgtcac agggcaggcc tgaagaactc tgcttcagc ttgcagctt tggtatgag	1662
gcctgaatac cgcagcaaaa tagatgccaa atacaaaaag aagatcgagg gaatggtcag	1722
gagacccgat atatctgaga tagaagaggg cacgactcca tgtccattct gcaaatttct	1782
tctcccagag agagaactcc tca	1805

<210> 8
 <211> 1523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (231)..(1202)

<400> 8

tattttgaag ctgtttaccc tcgcagctct ctgactggca cccctgcctg cctgccccgc

60

cctgcacaac atgcagccct ccggcctcga gggtcccgac acgttggtc ggtggccctct	120		
gctgagtctg ctgctcctgc tgctgctgct ccagcctgta acctgtgcct acaccacgcc	180		
aggccccccc cagagccctc accacgctgg gcgcccccag agcccacacc	atg ccg		
	Met Pro		
	1		
ggc acc tac gct ccc tcg acc aca ctc agt agt ccc agc acc cag ggc	284		
Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser Thr Gln Gly			
5	10	15	
ctg caa gag cag gca cgcc ctg atg cggt gac ttc ccgt ctc gtg gac	332		
Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe Pro Leu Val Asp			
20	25	30	
ggc cac aac gac ctg ccc ctg gtc cta agg cag gtt tac cag aaa ggg	380		
Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln Val Tyr Gln Lys Gly			
35	40	45	50
cta cag gat gtt aac ctg cgc aat ttc agc tac ggc cag acc agc ctg	428		
Leu Gln Asp Val Asn Leu Arg Asn Phe Ser Tyr Gly Gln Thr Ser Leu			
55	60	65	
gac agg ctt aga gat ggc ctc gtg ggc gcc cag ttc tgg tca gcc tat	476		
Asp Arg Leu Arg Asp Gly Leu Val Gly Ala Gln Phe Trp Ser Ala Tyr			
70	75	80	
gtg cca tgc cag acc cag gac cggt gat gcc ctg cgc ctc acc ctg gag	524		
Val Pro Cys Gln Thr Gln Asp Arg Asp Ala Leu Arg Leu Thr Leu Glu			
85	90	95	
cag att gac ctc ata cgc cgc atg tgt gcc tcc tat tct gag ctg gag	572		
Gln Ile Asp Leu Ile Arg Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu			
100	105	110	
ctt gtg acc tcg gct aaa gct ctg aac gac act cag aaa ttg gcc tgc	620		
Leu Val Thr Ser Ala Lys Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys			
115	120	125	130
ctc atc ggt gta gag ggt ggc cac tcg ctg gac aat agc ctc tcc atc	668		
Leu Ile Gly Val Glu Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile			
135	140	145	
tta cgt acc ttc tac atg ctg gga gtg cgc tac ctg acg ctc acc cac	716		
Leu Arg Thr Phe Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His			
150	155	160	
acc tgc aac aca ccc tgg gca gag agc tcc gct aag ggc gtc cac tcc	764		
Thr Cys Asn Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser			
165	170	175	
ttc tac aac aac atc agc ggg ctg act gac ttt ggt gag aag gtg gtg	812		
Phe Tyr Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val			
180	185	190	

gca gaa atg aac cgc ctg ggc atg atg gta gac tta tcc cat gtc tca 860
 Ala Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
 195 200 205 210

 gat gct gtg gca cg^g cg^g gcc ctg gaa gtg tca cag gca cct gtg atc 908
 Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val Ile
 215 220 225

 ttc tcc cac tcg gct gcc cg^g ggt gtg tgc aac agt gct cg^g aat gtt 956
 Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg Asn Val
 230 235 240

 cct gat gac atc ctg cag ctt ctg aag aag aac ggt ggc gtc gtg atg 1004
 Pro Asp Asp Ile Leu Gln Leu Lys Lys Asn Gly Gly Val Val Met
 245 250 255

 gtg tct ttg tcc atg gga gta ata cag tgc aac cca tca gcc aat gtg 1052
 Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro Ser Ala Asn Val
 260 265 270

 tcc act gtg gca gat cac ttc gac cac atc aag gct gtc att gga tcc 1100
 Ser Thr Val Ala Asp His Phe Asp His Ile Lys Ala Val Ile Gly Ser
 275 280 285 290

 aag ttc atc ggg att ggt gga gat tat gat ggg gcc ggc aag tac agg 1148
 Lys Phe Ile Gly Ile Gly Asp Tyr Asp Gly Ala Gly Lys Tyr Arg
 295 300 305

 aag aaa aca aag tgc aaa gcc cct tgg agg aca agt tcc cg^g atg agc 1196
 Lys Lys Thr Lys Cys Lys Ala Pro Trp Arg Thr Ser Ser Arg Met Ser
 310 315 320

 agc tga gcagttcctg ccactccgac ctctcacgtc tgcgtcagag acagagtctg 1252
 Ser *

 acttcaggcc aggaactcac tgagattccc atacactgga cagccaagtt accagccaag 1312
 tggcagtc cagagtccctc cccccacatg gccccagtcc ttgcagttgt ggccaccttc 1372
 ccagtcctta ttctgtggct ctgatgaccc agttagtcct gccagatgtc actgttagcaa 1432
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 gttttggaca tagaaacaga aaaaaaaaaa a 1523

<210> 9
 <211> 1608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)...(1608)

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agc atc aat aaa tcc ggg gcc tct tat gag aag atc aaa gaa gtg att Ser Ile Asn Lys Ser Gly Ala Ser Tyr Glu Lys Ile Lys Glu Val Ile 230 235 240	777
ggt cat ggt tgt aaa tgg acg ctc agc aga ttt ttt tcc tac ctt cgt Gly His Gly Cys Lys Trp Thr Leu Ser Arg Phe Phe Ser Tyr Leu Arg 245 250 255	825
agc tgg gat gtg gac gat ctg ctt ttg tgg aag aaa atc cac cgc atg Ser Trp Asp Val Asp Asp Leu Leu Leu Trp Lys Lys Ile His Arg Met 260 265 270 275	873
gtt att ctc acc att ctc gcc att gca cca tct gtc ccc ttt gct gcc Val Ile Leu Thr Ile Leu Ala Ile Ala Pro Ser Val Pro Phe Ala Ala 280 285 290	921
aat tgc ttt gag ctc ttt ggg ttt gat att ttg att gat gac aac ttg Asn Cys Phe Glu Leu Phe Gly Phe Asp Ile Leu Ile Asp Asp Asn Leu 295 300 305	969
aaa cca tgg ctt tta gag gtc aac tac agc cca gcc ttg acc ttg gat Lys Pro Trp Leu Leu Glu Val Asn Tyr Ser Pro Ala Leu Thr Leu Asp 310 315 320	1017
tgt tca aca gat gtg ttg gtg aag aga aaa ctt gtc cat gat att att Cys Ser Thr Asp Val Leu Val Lys Arg Lys Leu Val His Asp Ile Ile 325 330 335	1065
gac ctg att tac tta aat ggt cta aga aat gag ggg aga gaa gcc agt Asp Leu Ile Tyr Leu Asn Gly Leu Arg Asn Glu Gly Arg Glu Ala Ser 340 345 350 355	1113
aat gcc aca cat gga aat tcc aac atc gac gct gca aaa agt gac aga Asn Ala Thr His Gly Asn Ser Asn Ile Asp Ala Ala Lys Ser Asp Arg 360 365 370	1161
ggt ggg ctt gat gct cct gac tgt ctt cct tat gat tct ctt tcg ttc Gly Gly Leu Asp Ala Pro Asp Cys Leu Pro Tyr Asp Ser Leu Ser Phe 375 380 385	1209
aca agc aga atg tac aac gag gat gac tct gtg gtg gag aaa gct gtg Thr Ser Arg Met Tyr Asn Glu Asp Asp Ser Val Val Glu Lys Ala Val 390 395 400	1257
agt gtg cgt cct gaa gct gca cct gcc tcc cag ctg gaa gga gag atg Ser Val Arg Pro Glu Ala Ala Pro Ala Ser Gln Leu Glu Gly Glu Met 405 410 415	1305
agt ggg cag gat ttt cat ctg tca aca agg gag atg cca caa agc aag Ser Gly Gln Asp Phe His Leu Ser Thr Arg Glu Met Pro Gln Ser Lys 420 425 430 435	1353

ccc aag tta cgg agc agg cac acg cct cac aag aca ctc atg ccc tac Pro Lys Leu Arg Ser Arg His Thr Pro His Lys Thr Leu Met Pro Tyr 440 445 450	1401
gcg tcc ctc ttc cag tcg cac tcc tgc aag acc aag acc tcc ccg tgt Ala Ser Leu Phe Gln Ser His Ser Cys Lys Thr Lys Thr Ser Pro Cys 455 460 465	1449
gtc ctg tca gac cgt ggc aaa gct cca gat ccc caa gca ggc aac ttt Val Leu Ser Asp Arg Gly Lys Ala Pro Asp Pro Gln Ala Gly Asn Phe 470 475 480	1497
gtt ctt gtt ttt cct ttc aat gaa gca act ctc gga gct tcc agg aat Val Leu Val Phe Pro Phe Asn Glu Ala Thr Leu Gly Ala Ser Arg Asn 485 490 495	1545
gga tta aat gtc aaa aga ata atc caa gag ctc cag aaa cta atg aat Gly Leu Asn Val Lys Arg Ile Ile Gln Glu Leu Gln Lys Leu Met Asn 500 505 510 515	1593
aag caa cat tcc taa Lys Gln His Ser * 520	1608

<210> 10
 <211> 1891
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (362)..(1084)

<220>
 <221> misc_feature
 <222> (1)..(1891)
 <223> n = a,t,c or g

<400> 10

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gagggtgtga tggagtgat tggaaatatt gcagccctgc atagtctcca tcagggatgt 120
gacaaagtgg ataatctcta ccacgtgaga aacttccaaac attacttgca aatcagattt 180
aatgaataaaa ataaagctgt agcacttggc acattcattt ggacccttac ccaaaccattt 240
tcaatattgt gtacgttatac tttattatca ggtcacaaaa gatgtcataa aagaatttgc 300
agatgacggc gtcaagtacc tggactaag gagcacaccc agaagagaaa atgctactgg 360
a atg act aaa aag act tat gtg gaa tct ata ctt gaa ggt ata aaa Met Thr Lys Lys Thr Tyr Val Glu Ser Ile Leu Glu Gly Ile Lys 406

1	5	10	15	
cag tcc aaa caa gaa aac ttg gac att gat gtt agg tat ttg ata gca				454
Gln Ser Lys Gln Glu Asn Leu Asp Ile Asp Val Arg Tyr Leu Ile Ala				
20	25	30		
gtt gac aga aga ggt ggc cct tta gta gcc aag gag act gta aaa ctt				502
Val Asp Arg Arg Gly Gly Pro Leu Val Ala Lys Glu Thr Val Lys Leu				
35	40	45		
gcc gag gag ttc ttc ctt tct act gag ggt aca gtt ctt ggc ctt gac				550
Ala Glu Glu Phe Phe Leu Ser Thr Glu Gly Thr Val Leu Gly Leu Asp				
50	55	60		
ctc agt gga gac cct act gta gga caa gca aaa gac ttc ttg gaa cct				598
Leu Ser Gly Asp Pro Thr Val Gly Gln Ala Lys Asp Phe Leu Glu Pro				
65	70	75		
ctt tta gaa gct aag aaa gca ggt ctg aag tta gca ttg cat ctt tca				646
Leu Leu Glu Ala Lys Ala Gly Leu Lys Leu Ala Leu His Leu Ser				
80	85	90	95	
gag att cca aac caa aaa gaa aca caa ata ctc ctg gat ctg ctt				694
Glu Ile Pro Asn Gln Lys Lys Glu Thr Gln Ile Leu Leu Asp Leu Leu				
100	105	110		
cct gac aga atc ggg cat gga aca ttt ctc aac tcc ggt gag gga gga				742
Pro Asp Arg Ile Gly His Gly Thr Phe Leu Asn Ser Gly Glu Gly Gly				
115	120	125		
tcc ctg gat ctg gtg gac ttt gtg agg caa cat cgg ata cca ctg gaa				790
Ser Leu Asp Leu Val Asp Phe Val Arg Gln His Arg Ile Pro Leu Glu				
130	135	140		
ctc tgt ttg acc tca aac gtc aaa agt cag aca gtt cca tct tat gac				838
Leu Cys Leu Thr Ser Asn Val Lys Ser Gln Thr Val Pro Ser Tyr Asp				
145	150	155		
cag cac cat ttc gga ttc tgg tac agc att gcc cat cct tct gtg atc				886
Gln His His Phe Gly Phe Trp Tyr Ser Ile Ala His Pro Ser Val Ile				
160	165	170	175	
tgt act gat gat aag ggt gtt ttt gca aca cac ctt tct caa gag tac				934
Cys Thr Asp Asp Lys Gly Val Phe Ala Thr His Leu Ser Gln Glu Tyr				
180	185	190		
cag ctg gca gct gaa aca ttt aat ttg acc cag tct cag gtg tgg gat				982
Gln Leu Ala Ala Glu Thr Phe Asn Leu Thr Gln Ser Gln Val Trp Asp				
195	200	205		
ctg tct tat gaa tcc atc aac tac atc ttt gct tct gac agc acc aga				1030
Leu Ser Tyr Glu Ser Ile Asn Tyr Ile Phe Ala Ser Asp Ser Thr Arg				
210	215	220		
tct gaa ctg agg aag aaa tgg aat cac ctg aag ccc aga gtg tta cat				1078
Ser Glu Leu Arg Lys Lys Trp Asn His Leu Lys Pro Arg Val Leu His				
225	230	235		

att taa gctataatga ggtgaactac ttctgagttat gtgtttcaat caagttcctg 1134
Ile *
240

ccatatccca ctttagtaaaa cagtcacca ctccttgaa gcatagcaac caagttcctt 1194
gggctctatc accagcacct tacacatggc aggtactcag taaatacgtg tcttcaactg 1254
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